protein

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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267
1 LAKAGFYYIGPCDPV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    219241 seqs, 76174552 residues
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GenCore version
Copyright (c) 1993 - 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LAKAGFYYIGPGDRVACFAC.....
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  80
                                                                            A45478
A45478
T10304
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T141814
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S69544
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Compugen
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34.394 Million cell updates/sec
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                                                                 apoptosis inhibitor - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Species: Sus scrofa domestica (domestic pig)
C:Species: O4-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 02-Sep-2000
C:Accession: JC5964
R:Stehilk, C: de Martin, R.; Binder, B.R.; Lipp, J.
Biochem. Biophys. Res: Commun. 243, 827-832, 1998
A:Title: Cytokine induced expression of porcine inhibitor of apoptosis protein (A; Reference number: JC5964; MUID:98162622
A; Reference number: JC5964
A; Status: preliminary
A; Molecule type: DNA
A:Residues: 1-358 <97E>
A; Cross-references: GB:U79142; NID:92957174; PIDN:AAC39171.1; PID:92957175
C:Superfamily: RING finger homology
F; 307-351/Domain: RING finger homology <RRN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      apoptosis inhibitor hiap-1 - human c;Species: Homo sapiens (man) c;Species: Homo sapiens (man) c;Pate: 17-Jul-1998 *sequence_revision 17-Jul-1998 *text_change 21-Jul-2000 c;Accession: S68449 ramai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Faraha R:Title: Suppression of apoptosis in mammalian cells by NAIP and a related family of A;Accession: S68449 MJD:96149249 A;Accession: S68449 A;Accession: S68449 A;Accession: S68449 Residues: nucleic acid sequence not shown A,Molecule type: mRNA A;Accession: S6844 CLIS-A;Accession: S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Description: apoptotic suppressor
C; Superfamily: RING finger homology
C; Keywords: apoptosis; zinc finger
C; F; 553-597/Domain: RING finger homology <RNG>
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S68449
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JC5964
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:U45878; NID:g1184315; PIDN:AAC50371.1; PID:g1184316
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Best Local Similarity 97.8
Matches 45; Conservative
Query Match
Best Local Similarity
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93.5%;
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C2494

UH0470

T02534

T47287

T477287

T477287

A81807

A81807

A81807

A81807

A81807

A81807

A81807

T34035

A27340

T34035

A27340

T34035

A284040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 264; DB 2; Length 604; Pred. No. 8.3e-25; 1; Mismatches 0; Indels
  Score 254; DB 2; Pred. No. 8.7e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALIGNMENTS
                                                                                                                                                                                                                               inhibitor of apoptosis protein (iap)
                     Length 358;
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hypothetical prote
env polyprotein -
Zinc finger, C3HC4
ring-infected eryt
ATP-dependent heli
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Na+/K+-exchanging
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0 Gaps

9

Result No.

Query Match

222223456756999 2222235734567596999 2222357345675969391 2222354567569391

Total number of

Database

Scoring table: Sequence: Title: Perfect score: Run on:

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A.Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-497 CDUC>
A:Cross-references: EMBL:U32974; NID:g1016687; PIDN:AAC50518.1; PID:g1016688
R:Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.;
Nature 379, 349-353, 1996
A:Title: Suppression of apoptosis in mammalian cells by NAIP and a related fami
A:Reference number: A58182; MUID:96149249
A:Accession: S68451
A:Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 apoptosis inhibitor hiap-2 - human c;Species: Homo sapiens (man) C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 21-Jul-2000 C;Accession: $68450 R;ILISTON, P; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Farahar Nature 379, 349-353, 1996 A;Title: Suppression of apoptosis in mammalian cells by NAIP and a related family of 3 A;Reference number: A58182; MUID:96149249 A;Accession: $68450 A;Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                    A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-161,'C',163-422,'O',424-497 <LIS>
A;Cross-references: EMBL:U45880; NID:g1184319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            apoptosis inhibitor IAP homolog - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 06-Dec:1996 #sequence_revision 13-Mar-1997 #text_change 17-Nov-2000 C;Accession: S69544; S68451 R;Duckett, C.S.; Nava, V.E.; Gedrich, R.W.; Clem, R.J.; van Dongen, J.L.; Gilfillan, M. EMBO J. 15, 2685-2694, 1996 A;Tittle: A conserved family of cellular genes related to the baculovirus iap gene and e A;Reference number: S69544; MUID:96256286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Description: apoptotic suppressor C; Superfamily: RING finger homology C; Keywords: apoptosis; zinc finger F;567-611/Domain: RING finger homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: mRNA
A;Residues: 1-618 <LIS>
A;Cross-references: EMBL:U45879; NID:g1184317;
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                                                                                    Description: apoptotic suppressor; Superfamily: apoptosis inhibitor IAP homolog; Keywords: apoptosis; zinc finger; 446-490/Domain: RINC finger homology <RRN>
     Query Match
Best Local Similarity
                                                                                                                                                                                                                                  Genetics:
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Best Local Similarity 91.3
Matches 42: Conservative
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     68.2%;
69.6%;
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Pred. No. 7.9e-23;
2; Mismatches 2;
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     Score 182; DB 2; pred. No. 8.7e-15;
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                                                                                                                                                                                                                                                    PIDN:AAC50373.1; PID:g1184320
                                                                                                                                                                                                                                                                                                                                                                                      cells by NAIP and a related family of IAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIDN:AAC50372.1; PID:g1184318
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                         Length 497;
                                                                                                                                       finger homology
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apoptosis inhibitor diap - fruit fly (Drosophila melanogaster)
C;Species; Drosophila melanogaster
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 17-Nov-2000
C;Accession: S68452; S78528
R;Liston, P.; Roy, N.; Tamal, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Faraha
Nature 379, 349-353, 1996
Nature 379, 349-353, 1996
A;Fitle: Suppression of apoptosis in mammalian cells by NAIP and a related family of
A;Accession: S68452
A;Accession: S68452
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-496 CLIS-
A;Residues: 1-496 CLIS-
A;Residues: 1-496 CLIS-
A;Residues: Teach control of the clist control of the clist
                                                                                                                                                                                                                                                                                                                                                                                apoptosis inhibitor IAP homolog - fruit fly (Drosophila melanogaster) C;Species: Drosophila melanogaster C;Species: Drosophila melanogaster C;Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000 C;Accession: S69545 R;Duckett, C.S.; Nava, V.E.; Gedrich, R.W.; Clem, R.J.; van Dongen, J.L.; Gilfillan, EMBO J. 15, 2685-2694, 1996 PMBO J. 15, 2685-2694, 1996 PMBO J. 15, 2685-2694, MUID:96256286
C;Superfamily: apoptosis inhibitor IAP homolog; RING finger homology F;446-490/Domain: RING finger homology <RRN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Description: apoptotic suppressor
C;Superfamily: apoptosis inhibitor IAP homolog:
C;Keywords: apoptosis; zinc finger
F;445-489/Domain: RING finger homology <RNG>
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A;Residues: 1-36,'AT',37,'K',39,'L',41-44,'H',46-58,'Q',60-412,'A',414-427,'A',429-49
A;Cross-references: EMBL:U45881; NID:g1184313; PIDN:AAC48988.1; PID:g1184314
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S68452
                                                                                                                                                                                                                     A;Status: preliminary; nucleic acid sequence
A;Molecule type: mRNA
A;Residues: 1-497 <DUC>
                                                                                                                                                                                                                                                                                                                                                   A; Reference number: A; Accession: S69545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Genetics:
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A;Reference number: S78528
A;Accession: S78528
                                                                                                                                                                     A;Cross-references: EMBL:U32373; NID:gl019116; PIDN:AAC47155.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references: FlyBase: FBgn0015247
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                                                                                                                                   Genetics:
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 LAKAGFYYIGPGDRVACFACGGKLSNWEPKDNAMSEHLRHFPXCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 LAKAGFYYIGPGDRVACFACGGKLSNWEPKDNAMSEHLRHFPKCPF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54.38;
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Pred. No. 3.2e-10;
4; Mismatches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                   not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                            baculovirus iap gene and
                                                                                                                                                                         PID:g1019117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PID: 91184314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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Similarity
Conservative
         5 5
        68;
4
Score 145; DB 2;
Pred. No. 3.2e-10;
; Mismatches 16
              Length 497;
Indels
0
Gaps
0;
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1 LAKAGFYYIGPGDRVACFACGGKLSNWEPKDNAMSEHLRHFPKCP 45

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R;Roy, N.; Mahadevan, M.S.; McLean, M.; Shutler, G.; Yaraghi, Z.; Farahani, R.; d, T.O.; de Jong, P.J.; Surh, L.; Ikeda, J.E.; Korneluk, R.G.; MacKenzie, A. Cell 80, 167-178, 1995
A;Title: The gene for neuronal apoptosis inhibitory protein is partially deleted A; Reference number: A55478; MUID:95112344
A; Accession: A55478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GDB:120378: OMIM:600354; OMIM:253300
A;Map position: 5q12.2-5q13
C;Keywords: apoptosis; ATP; glycoprotein; nucleotide binding; p-loop; trans
E;94-110/Domain: transmembrane *status predicted <TMM1>
E;470-477/Region: nucleotide-binding motif A (P-loop)
E;479-496/Domain: transmembrane *status predicted <TMM2>
E;479-496/Domain: transmembrane tratus predicted
E;478-Binding site: ATP (Lys) *status predicted
E;618,632,823,923,1035/Binding site: carbohydrate (Asn) (covalent) *status
                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Accession: T42628
R; Yaraghi, Z.; Diez, E.; Gros, P.; MacKenzie, A.
R; Yaraghi, Z.; Diez, E.; Gros, P.; MacKenzie, A.
R; Yatraghi, Z.; Diez, E.; Gros, P.; MacKenzie, A.
A; Title: CDNA cloning and the 5'genomic organization
A; Title: CDNA cloning and the 5'genomic organization
A; Active country in the 5'genomic organization
A; Accession: T42628
A; Accession: T42628
A; Machecule type: mRNA
A; Residues; 1-1447 < YARP
A; Residues; 1-1447 < YARP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-1232 <ROY>
A; Cross-references: GB:U19251
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Homo sapiens (man)
C;Date: 05-Jan-1996 *sequence_revision 05-Jan-1996 *text_change 02-Feb-2001
C;Accession: A55478
                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references:
C;Genetics:
A;Gene: Naip2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neuronal apoptosis inhibitory protein 2 - mouse
C;Species: Mus musculus (house mouse)
C;Date: II-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
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inhibitor of apoptosis protein 3 - Orgyia pseudotsugata nuclear polyhedrosis virus C; Species: Orgyia pseudotsugata nuclear polyhedrosis virus, OpMNPV
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Best Local S
Matches 24
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Best Local S
Matches 24
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                                                                                                                                                       181 LSAAGEVETGKRDTVQCESCGGCLGNWEEGDDPWKEHAKWFPKCEF 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              299 LAKAGLEYTGIKDIYQCFSCGGCLEKWQEGDDPLDDHTRCFPNCPF 344
                                                                                                                                                                                                        μ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 LAKAGFYYIGPGDRVACFACGGKLSNWEPKDNAMSEHLRHFPKCPF 46
                                                                                                                                                                                    LAKAGFYYIGPGDRVACFACGGKLSNWEPKDNAMSEHLRHFPKCPF 46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL:AF102871; NID:g3860228; PID:g3860229; PIDN:AAC73002.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52.8%;
                                                                                                                                                                                                                                                                                 51.7%;
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                                                                                                                                                                                                                                                                              Score 138; DB 2;
Pred. No. 6.3e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16;
                                                                                                                                                                                                                                                                                                     Length 1447;
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Query Match

49.18;

Score 131;

DB 2;

Length 275

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R.Birnbaum, M.J.; Clem, R.J.; Miller, L.K.
J. Virol. 68, 2521-2528, 1994
A.Title: An apoptosis inhibiting gene from a nuclear polyhedrosis virus 6
A.Feference number: A53989; MUID:94187094
A.Fecession: A53989
A.Fecession: Preliminary
A.Fecession: Freilminary
A.Fesidues: Preliminary
A.Fesidues: Preliminary
A.Fesidues: 1-268 CBIR>
A.Fesidues: 1-268 CBIR>
A.Fesidues: 1-268 CBIR>
A.Foot: authors translated the codon TGG for residue 28 as Tyr, GAC for 1 C:Superfamily: Viral apoptosis inhibitor IAP; RING finger homology
F;217-261/Domain: RING finger homology <RRN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Date: 16-Jul-1999 *sequence_revision 16-Jul-1999 *text_change 15-Sep-2000 C;Accession: T10304
R;Ahrens, C.A.; Russell, R.R.; Funk, C.J.; Evans, J.; Harwood, S.; Rohrmann Virology 229, 381-399, 1997
A;Title: The sequence of the Orgyia pseudotsugata multinucleocapsid nuclear A;Reference number: Z17011; MUID:97271300
A;Accession: T10304
A;Status: preliminary; translated from GB/EMBL/DDBJ
Inhibitor-of-apoptosis polypeptide (IAP) - Cydia pomonella granulosis virus CpGV C;Species; Cydia pomonella granulosis virus CpGV C;Species; Cydia pomonella granulosis virus CpGV C;Date: 21-Sep-193 *sequence_revision 25-Apr-1997 *text_change 15-Sep-2000 C;Accession: A45679 R;Crook, N.E.; Clem, R.J.; Miller, L.K.
J. Virol. 67, 2168-2174, 1933
A:Title: An apoptosis-inhibiting baculovirus gene with a zinc finger-like motif. A, Reference number: A45679; MUID:93188168
A;Recession: A45679
A;Status: preliminary
A;Molecule: type: DNA
A;Residues: 1-275 CCRO>
A;Residues: 1-275 CCRO>
A;Cross-references: GB:L05494; NID:9289583; PIDN:AAA43835.1; PID:9289584
A;Cross-references: GB:L05494; NID:9289583; PIDN:AAA43835.1; PID:9289584
A;Cross-references: GB:L05494; NID:9289583; PIDN:AAA43835.1; PID:9289584
A;Note: Sequence extracted from NCBI backbone (NCBIN:127014, NCBIP:127015)
C;Superfamily: viral apoptosis inhibitor IAP; RING finger homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           apoptosis-inhibiting protein - Orgyla pseudotsugata multicapsid nuclear polyhedrosis C;Species: Orgyla pseudotsugata multicapsid nuclear polyhedrosis virus, OpMNPV C;Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 15-Sep-2000 C;Accession: A53989
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C;Superfamily: viral apoptosis inhibitor IAP; RING finger homology
F;217-261/Domain: RING finger homology <RRN>
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A; Residues: 1-268 < AHR>
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Conserv
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Best Local Similarity
Matches 21; Conserv
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Pred. No. 3e-09;
8; Mismatches 17
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C;Genetics:
A;Gene: kiap
A;Map position: 2
C;Keywords: apopt
probable apoptosis inhibitor - Chilo iridescent virus C;Species: Chilo iridescent virus C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #t C;Accession: T03183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kidney inhibitor of apoptosis protein - human C;Species: Homo sapiens (man) G;Date: 31-Mar-2001 #sequence_revision 31-Mar-2001 #text_change 31-Mar-2001 C;Date: 31-Mar-2001 #sequence_revision 31-Mar-2001 #sequence_revi
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J. Cell Biol. 141, 1415-1422, 1998
A; Title: A glant ubiquitin-conjugating enzyme related to TAP apoptosis inhibi
A; Reference number: Z20963; MUID:98292517
A; Accession: T91067
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-4845 < CHAU
A; Cross-references: EMBL:Y17267; NID:g3319989; PIDN:CAA76720.1; PID:g3319990
A; Note: localized to the Gold1 compartment and the vesicular system
C; Keyword9: membrane-associated protein
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A;Molecule type: mRNA
A;Residues: 1-298 <LIN>
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Pred. No. 1.6e-06;
3; Mismatches 19;
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                                   24-Mar-1999 #text_change 02-Sep-2000
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smatches 17;
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Search completed: Job time: 704 sec

January

7, 2002,

15:49:10

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A; Molecule type: DNA
A; Residues: 1-997 <HAN>
A; Cross references: EMBL: AL031323; PIDN:CAA20434.1; GSI
A; Cross references: EMBL: AL031323; PIDN:CAA20434.1; GSI
A; Experimental source: Strain 972h: cosmid c952
R; Wedler, H; Duesterhoeft, A: McDougall, R.C.; Rajanc
submitted to the EMBL Data Library, October 1999
A; Reference number: Z22010
A; Accession: T41700
A; Status: translated from GB/EMBL/DDBJ
A; Residues: 912-97 <MED>
A; Residues: 912-97 <MED>
A; Cross-references: EMBL: AL121859; PIDN:CAB58376.1; GSI
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Cutl7 protein - fission yeast (Schizosacharomyces | Cutl7 protein - fission yeast (Schizosacharomyces pombe C; pate: 21-Jan-2000 *sequence_revision 21-Jan-2000 C; Accession: T43523; T41649; T41700

C; Accession: T43523; T41649; T41700

R; Morishita, J; Matsusaka, T; Yanagida, M. submitted to the EMBL Data Library, August 1999

A, Description: Fission yeast cutl7 is required for A; Reference number: Z22536
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Virus Genes 15, 235-245, 1997
A;Title: The DNA sequence of Chilo iridescent virus between the genome coordinates A;Reference number: Z14834; MUID:98141693
A;Recession: T03183
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-208 <BAH>
A;Residues: 1-208 <BAH>
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A; Residues: 1-997 < MOR>
A; Residues: 1-997 < MOR>
A; Cross-references: EMBL: AB031034; PIDN: BAA83415.1
R; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell,
A; Reference number: Z22007
A; Accession: T41649
                                                                                                                                                                                                                                 C;Genetics:
A;Gene: cutl7; SPCC962.02c; SPDB:SPCP31B10.10c
A;Map position: 3L
A;Introns: 43/3
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C;Superfamily: RING finger homology
F;159-202/Domain: RING finger homology <RRN>
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Best Local Similarity
Matches 20; Conserv
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Best Local Similarity 47.5%;
Matches 19; Conservative
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                                 LAKAGFYY--IGPG-----DRVACFACGGKLSNWEPKDNAMSEHLRHFPKCPF 45
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                                                                                                             Conservative
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Pred. No. 1.6e-06;
6; Mismatches 15;
                                                                                                       Score 103; DB 2; I Pred. No. 9.1e-05; 6; Mismatches 20;
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